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 US-08-252-384C-2
 ; Sequence 2, Application US/08252384C
 ; GENERAL INFORMATION:
   APPLICANT: Reactive Surfaces, Ltd.
   APPLICANT: McDaniel, Steven
   APPLICANT: Raushel, Frank M
   APPLICANT: Wild, James R
   TITLE OF INVENTION: Recombinant Organophosphorous Acid Anhydrase and Methods
 of Use
   FILE REFERENCE: TAMK145
   CURRENT APPLICATION NUMBER: US/08/252,384C
   CURRENT FILING DATE: 1994-06-01
   PRIOR APPLICATION NUMBER: US 07/928,540
   PRIOR FILING DATE: 1992-08-13
   PRIOR APPLICATION NUMBER: US 07/344,258
   PRIOR FILING DATE: 1989-04-27
   NUMBER OF SEQ ID NOS: 2
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  CURRENT FILING DATE: 1994-06-01
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  APPLICANT: McDaniel, C. Steven
  TITLE OF INVENTION: Recombinant Organophosphorus Acid Anhydrase and Methods
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  FILE REFERENCE: RACT-00200
  CURRENT APPLICATION NUMBER: US/08/252,384A
  CURRENT FILING DATE: 2004-06-01
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  PRIOR FILING DATE: 1992-08-13
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  PRIOR FILING DATE: 1994-06-01
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  FILE REFERENCE: RACT-00100
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  CURRENT FILING DATE: 1994-06-01
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    TITLE OF INVENTION: PARATHION HYDROLASE ANALOGS AND METHODS
; FOR PRODUCTION AND PURIFICATION
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     FILING DATE: 25-JUN-1992
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	gac gt Asp Va	c agt 1 Ser	tta Leu	ttg Leu 85	gcc Ala	gag Glu	gtt Val	tcg Ser	cgg Arg 90	gct Ala	gcc Ala	gac Asp	gtt Val	cat His 95	atc Ile	2	88
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	agg ag Arg Se	t gta r val	gag Glu	gaa Glu	ctc Leu	aca Thr	cag Gln	ttc Phe	ttc Phe	ctg Leu	cgt Arg	gag Glu	att Ile	caa Gln	tat Tyr	3	84

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atc Ile	act Thr	gtg Val	act Thr	aac Asn 325	ccg Pro	gcg Ala	cgg Arg	ttc Phe	tat Tyr 330	gtc Val	acc Thr	gac Asp	ctt Leu	gcg Ala 335	ggc Gly	1008
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Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val 275 280 285

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val 290 295 300

Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly 305

Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly 325 330 335

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<120> Title: Recombinant Organophosphorus Acid Anhydrase and Methods of Use

<140> CurrentAppNumber : Unknown <141> CurrentFilingDate : 2003-01-02

Earlier Applications

<150> PriorAppNumber : 07/928,540 <151> PriorFilingDate : 1992-08-13

Earlier Applications

<150> PriorAppNumber : 08/252,384 <151> PriorFilingDate : 1994-06-01

Earlier Applications

<150> PriorAppNumber : 07/344,258

<151> PriorFilingDate : 1989-04-27

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RACT00200 2nd Amd Seq Listing.WorkFile

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McDaniel, C. Steven

<120> Recombinant Organophosphorus Acid Anhydrase and Methods of Use

<130> RACT-00200

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<151> 1992-08-13

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Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala 50 55 60

Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg 65 70 75 80

Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile 85 90 95

Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu 100 105 110

Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr 115 120 125

RACT00200 Sequence Listing

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Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp 195 200 205

Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu 210 215 220

Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala 225 230 235 240

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Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn 260 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val 275 280 285

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val 290 295 300

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Page 1

Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala

55

Ala Gly Val Arg Thr tle Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr Gly Leu Top Phe Asp Pro Pro Leu Ser Met Arg Leu 105 Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp Thr Gly Ile Art Ala Gly Ile Ile Lys Val Ala Thr 135 140 Thr Gly Lys Ala Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Ala 155 160 Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala 165 170 Ser Gln Arg Asp Gly Glu Gln Gln Ala Ala Ile Phe Glu Ser Glu Gly 180 Leu Ser Pro Ser Arg Val Cys Ile Gly Hid Ser Asp Asp Thr Asp Asp 195 Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Cly Tyr Leu Ile Gly Leu 210 220 Asp His Ile Pro His Ser Ala Ile Gly Leu Glt Asp Asn Ala Ser Ala 230 235 Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile 250

Page 2

Lys Ala Leu Ile Asp Gln Gly Tyr Met Lys Gln Ile Leu Val Ser Asn 260 270

Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val

Met Asp Arg Val Asn Pro Asp Gly Met Ala Phe Ile Pro Leu Arg Val 290 300

Ile Pro Phe Leu Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly 315 320

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Ser

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Reactive Surfaces, Ltd.

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Thr Ile Ser Glu Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly

MAY-21-2003 WED 10:12 AM

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25

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aaa got ota gog gaa aag got gtg aga gga ttg ogo ogo goo aga gog 192 Lys Ala Leu Ala Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala 50 55 60

get ggc gtg cga acg att gtc gat gtg tcg act ttc gat atc ggt cgc Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg 65 70 75 80

gac gtc agt tta ttg gcc gag gtt tcg cgg gct gcc gac gtt cat atc Asp Val Ser Leu Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile 85 90 95

gtg gog gog acc ggc ttg tgg ttc gac ccg cca ctt tcg atg cga ttg Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu 100 105 110

agg agt gta gag gaa ctc aca cag ttc ttc ctg cgt gag att caa tat 384 Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr 115 120 125

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ttg age eec tea egg gtt tgt att ggt eac age gat gat act gac gat Leu Ser Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp Asp

ttg age tat etc acc gee etc get geg ege gga tac etc atc ggt eta Leu Ser Tyr Leu Thr Ala Leu Ala Ala Arg Gly Tyr Leu Ile Gly Leu

gac cac atc ccg cac agt gcg att ggt cta gaa qat aat gcg agt gca Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn Ala Ser Ala

tca goo etc etg gge atc egt teg tgg caa aca egg get etc ttg atc

255

Ser Ala Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile 245 250

MCDAMEL AND ASSOCIATES

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gac tgg ctg ttc ggg ttt tcg age tat gtc ace aac ate atg gac gtg Asp Trp Leu Phe Gly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val 275

280 285

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ate cca tte gta ega gag aag gge gte cca cag gaa aeg etg gea gge Ile Pro Phe Val Arg Glu Lys Gly Val Pro Gln Glu Thr Leu Ala Gly 305 315 320 310

ate act gtg act aac eeg geg egg tte tat gtc ace gae ett geg gge 1008 Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly 325 330 335

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Ala Gly Val Arg Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg 70 80

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Val Ala Ala Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu 100

Arg Ser Val Glu Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr 115

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Ile Thr Val Thr Asn Pro Ala Arg Phe Tyr Val Thr Asp Leu Ala Gly 325 330 335

Val

M MCDr

MCDANTEL AND ASSOCIATES

Protein Comparisons Percent Identity

DNA Comparisons Percent Identity

McDaniel vs Wild Lab	57.8%	McDaniel vs Wild Lab	88.0%
McDaniel vs Serdar	59.5%	McDaniel vs Serdar	83.7%
Serdar vs Wild Lab	100%	Serdar vs Wild Lab	99.6%

McCaniel. pro Net Gin The Arg Arg Val Val Lou Lya See Aia Ala Alo Arg The Leu Luu Gly Gly Lou Ala Gly Cya Ala The Tep Leu Aap Arg 28 28 28 28 29 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20
Serdar.pro Nat Gin The Arq Arg Vol Val Lou Lys Ser Als Ala
Hodaniel. pro Sor Ale Gin Ale Met Arg Ser Tic Arg Ale Arg Wild Lab. PROTTE GIY TO THE ARGULY AS SET VIL ARGULY Pro 11c Thr IIe Ser Glu Ale Gly Pho Thr Leu Thr His Glu Rap Ile Ser Ale Wild Lab. PROTTE GIY TO COLY AND ARGULY ARGULY PRO 12c Thr IIe Ser Glu Ale Gly Pho Thr Leu Thr His Glu Rap Ile Ser Ale Ser Cys Val Leu Gly Gin Ers Ger Ser Val Ale Gly Pro The The Leu Thr His Glu Rap Wild Lab. PROTEC File Ale Arg Gin Rapper Ser Cys Val Leu Gly Gin Ers Ger Ser Val Ale Gly Pro Thr His Glu Rap Wild Lab. PROTEC File Ale Arg Gly Pro Liv Fire Ale Ale Gly Pro Thr The Gly Ers His Jay Ale Gly Try Ale Thr Gly Ser Cys Val Leu Gly Gin Ers Ger Ser Val Ale Gly Nor Arg Gly Ser Cys Val Leu Gly Gin Ers Ger Ser Val Ale Gly Nor Arg Gly Ser Cys Val Leu Gly Gin Ers Ger Ser Val Ale Gly Nor Arg Gly Ser Cys Val Leu Gly Ale Gly Ser His Jay Ale Gly Marg Gly Ser Cys Val Leu Gly Ser His Jay Ale Gly Marg Gly Hodaniel. pro Ile Ale Arg Gin Ser Gly Trp Arg Ale Ann Asp Cys Arg Cys Val Aep Phe Arg Tyr Arg Ser Arg Arg Gln Phe Ile Gly Arg Gly Pho 11. Wild Lab. PROAP Ale Arg Ale Arg Arg Ser Tyr Leu Ale Ale Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Het Arg Leu Arg Tyr Val Glu Glu Leu Thr 14. McDaniel. pro Ale Gly Cys Arg Arg Ser Tyr Leu Ale Ale Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Het Arg Leu Arg Tyr Val Glu Glu Leu Thr 14. McDaniel. pro Marg Ale Ale Yel Val Marg Phe Arn Met Ale Ser Lya Tyr Phe Asp Pro Pro Leu Ser Het Arg Leu Arg Ger Val Glu Glu Leu Thr 14. McDaniel. pro Marg Ale Marg Marg Marg Marg Phe Arn Met Ale Ser Lya Tyr Thr Gly Ile Arg Ale Gly Tie Ile Lya Val Ale Thr Thr Gly Lya Il McDaniel. pro Marg Ale Gly Cys Arg Arg Ser Arg Val Arg Phe Arn Met Ale Ser Lya Tyr Thr Gly Ile Arg Ale Gly Tie Ile Lya Val Ale Thr Thr Gly Lya Il McDaniel. pro Ale Thr Pro Phe Gln Glu Leu Val Leu Lya Ale Ale Arg Ale Arg Ale Gly Tie Ile Lya Val Ale Thr Thr His Thr Ale Ale Ser Il McDaniel. pro Ale Thr Pro Phe Gln Glu Leu Val Leu Lya Ale Ale Arg Ale Arg Ale Ser Leu Ale Thr Gly Val Pro Val Thr Thr His Thr Ale Ale Ser Il McDaniel. pro Gln Arg Asp Gly Gl
Wild Lab. PROGRADA Arg TITASH YE WILD ARGED PRO 11e Thr 11e Ser Glu Ala Gly Phe Thr Lau Thr His Glu Hid 11e War May 32 Serdor. Pro His rich Thr. Gly Keep Arg His Assurance Vill Arg Glix Pro 11e Thr 11e Ser Glu Ala Gly Phe Thr Lau Thr His Glu Hid 11e War May 32 Serdor. Pro His rich Thr. Gly Keep Arg His Assurance Vill Arg Glix Pro 11e Thr 11e Ser Glu Ala Gly Phe Thr Lau Thr His Glu Hid 11e War May 32 Serdor. Pro His Glab. Prof He Lix Ala Cly Thr. Gly War Arg Gly Ser Arg Ser Vai Ala Cln Ser Ser Ser Gly Lys Gly Cys Glu Arg 60 Serdor. Pro His Gly War Arg Gly Try Brown Arg May New You Fro Gly Ser Arg Ser Vai Ala Gly War Arg Vai Arg Gly May Arg Vai Arg Arg Gly Phe 11e Gly Arg Gly Pho 11e McDaniel. Pro 11e Ala Arg Ala Arg Arg Gly Arg Fro 12e War Arg Vai May Phe Arg Try Arg Ser Arg Arg Gln Phe 11e Gly Arg Gly Pho 11e McDaniel. Pro Ala Arg Arg Arg Ser Tyr Leu Ala Ala Thr Gly Leu Try Phe Arg Pro Pro Leu Ser Met Arg Leu Arg Tyr Vai Glu Glu Leu Thr 14e Wild Lab. PRO Arg Ala Arg Arg Arg Ser Tyr Leu Ala Ala Thr Gly Leu Try Phe Arg Pro Pro Leu Ser Met Arg Leu Arg Tyr Vai Glu Glu Leu Thr 14e Wild Lab. PRO Arg Ala Ala Arg Ala Gly May Ala Ala Ahr Gly Leu Try Phe Arg Pro Pro Leu Ser Met Arg Leu Arg Tyr Vai Glu Glu Leu Thr 14e Wild Lab. PRO Arg Ala Ala Ala Che Vai Ala Ala Thr Gly Leu Try Phe Arg Pro Pro Leu Ser Met Arg Leu Arg Tyr Vai Glu Glu Leu Thr 14e McDaniel. Pro 11e Vai Leu Pro Ala Vai Arg The Arn Met Ala Ser Lya Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lya Vai Ala Thr Thr Gly Lya 17e McDaniel. Pro 11e Arg Ala Gly Ile Ile Lya Vai Ala Thr Thr Gly Lya 17e McDaniel. Pro Phe Gln Glu Leu Vai Leu Lya Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Vai Pro Vai Thr Thr His Thr Ala Ala Ser 17e Serdar. Pro 11e Arg Ala Gly Glu Glu Gly May May Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Vai Pro Vai Thr Thr His Thr Ala Ala Ser 17e Serdar. Pro 11e Arg Ala Gly Gly Gly Gly Arg Fro Pro Pro Leu Ser Arg Vai Cya Ile Gly His Ser Arg Arg Thr Arg 22i M
Serdor.pro Serdor.pro Serdor.pro Ser
Serdor.pro Serdor.pro Serdor.pro Ser
Wild Lab. PROBLET AT A TAY THE LAW AND AND CASE
Serdar pro Ser Servate Liv Previous and Riv Pro Pro Glo Rose file Gly McDaniel pro Ile Alo Arg Glo Ser Gly Trp Arg Ala Asn Asp Cys Arg Cys Val Asp Phe Arg Tyr Arg Ser Arg Arg Glo Phe Ile Gly Arg Gly Phe 11. Wild Lab Pro Riv Ala Arg Ala Arg Ala Arg The Ile Val Ago Val And Tyr Phe Riv Liv Vay Asp Val Car Lew Law Ala Gly Var Arg The Ile Val Ago Val And Tyr Phe Riv Liv Vay Asp Val Car Lew Law Ala Gly Val Glo Clo Val And Car Tyr Phe Riv Liv Val Ago Val And The Phe Riv Liv Val And Car Tyr Phe Riv Liv Val Car Car Tyr Liv Glo Car Tyr Ile Car Tyr Phe App Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr 14. Wild Lab Pro Riv Ala Ala Riv Car Val Ala Ala Ala Thr Gly Leu Trp Phe App Pro Pro Leu Ser Met Arg Leu Arg Ger Val Glu Glu Leu Thr 14. McDaniel Pro Car Ala Ala Riv Car Val Arg Phe And Met Ala Ser Lya Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lya Val Ala Thr Thr Gly Lya 17. Wild Lab Pro Cal Tyr The Car Car Car Car Tyr Leu Hard Car Tyr Gly Liv Car Esp Thr Gly Ile Arg Ala Gly Ile Ile Lya Val Ala Thr Thr Gly Lya 14. McDaniel Pro Car Car Tyr Phe Glo Clu Leu Val Leu Lya Ala Ala Ala Arg Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20. McDaniel Pro Cal Arg Asp Cly Clu Car Car Car Car Tyr Pro Phe Leu Ser Fro Lya Leu Car Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20. McDaniel Pro Cal Arg Asp Cly Clu Car Car Car Car Tyr Pro Phe Cal Car
McDaniel.pro lie Alo Arg Gin Ser Gly Trp Arg Ala Asn Asp Cys Arg Cys Val Aep Phe Arg Tyr Arg Ser Arg Arg Gin Phe Ile Gly Arg Gly Phe 11. Wild Lan. PRO Arg Ala Arg Risk Ala Gly Var Arg Thr. Tie Wal. Asp Val Ser Var Ser Arg Phe Rep Als Risk Val Asp Val Ges Lev Lau Arg Cys Val Ges Ser Ser Arg Arg Arg Arg Arg Arg Ser Tyr Lev Ala Ala Thr Gly Lev Trp Phe Asp Pro Pro Lev Ser Met Arg Lev Arg Tyr Val Glu Glu Lev Thr 14. McDaniel.pro Ala Gly Cys Arg Arg Ser Tyr Lev Ala Ala Thr Gly Lev Trp Phe Asp Pro Pro Lev Ser Met Arg Lev Arg Tyr Val Glu Glu Lev Thr 14. McDaniel.pro Ala Gly Cys Arg Arg Ser Tyr Lev Ala Ala Thr Gly Lev Trp Phe Asp Pro Pro Lev Ser Met Arg Lev Arg Ser Val Glu Glu Lev Thr 14. McDaniel.pro Ala Gly Cys Arg Arg Ser Arg Ala Ala Ala Thr Gly Lev Trp Phe Asp Pro Pro Lev Ser Met Arg Lev Arg Ser Val Glu Glu Lev Thr 14. McDaniel.pro Ala Gly Cys Arg Arg Ser Arg Ala Ala Ala Thr Gly Lev Trp Phe Asp Pro Pro Lev Ser Met Arg Lev Arg Ser Val Glu Glu Lev Thr 14. McDaniel.pro Ala Gly Cys Arg Arg Ser Arg Ala Vol Arg Phe Asp Met Ala Ser Lys Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys 17. McDaniel.pro Ala Thr Pro Phe Gln Glu Lev Val Lev Lys Ala Ala Ala Arg Ala Ser Lev Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20. McDaniel.pro Ala Thr Pro Phe Gln Glu Lev Val Lev Lys Ala Ala Ala Arg Ala Ser Lev Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 17. Serdar.pro Ala Thr Pro Phe Gln Glu Lev Val Lev Lys Ala Ala Ala Arg Ala Ser Lev Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 17. Serdar.pro Ala Thr Pro Phe Gln Glu Lev Val Lev Lys Ala Ala Ala Arg Ala Ser Lev Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20. McDaniel.pro Gln Arg Aep Gly Glu Arg Gly Arg Pro Pro Phe Lev Ser Fro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Aep Aep Thr Aep 20. Serdar.pro Gln Arg Aep Gly Glu Arg Gly Arg Pro Pro Phe Lev Ser Cyt Gly Lev Ser Arg Val Cys Ile Gly His Ser Ala Phr Aep 20. Serdar.pro Gln Arg Aep Gly Glu Arg Arg Pro Pro Phe Met Ser Cyt Gly Lev Esp Pro Ser Arg Val Cys Ile Gly His Ser Aep Aep Th
Wild Lab. PROAFF Ala Arg Ris Ala Gly Wei Arg Thr. 16 Yei Agg Wei Arg Thr. 16 Yei Agg Wei Arg The Respect File No. Arg Ala Arg Ris Ala Gly Wei Arg Thr. 16 Yei Agg Wei Arg The Pho Ang Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr. 14. Wild Lab. PROAFF Vei Ala Ala Ala Thr Gly Leu Trp Pho Ang Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr. 14. Wild Lab. PROAFF Vei Ala Ala Ala Thr Gly Leu Trp Pho Ang Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr. 14. Serdar. pro Arg Ala Arg Ala Ser Vei Glu Glu Leu Thr. 14. McDaniel. pro Ala Val Leu Pro Ala Val Ala Ala Thr Gly Leu Trp Pho Ang Pro Pro Leu Ser Met Arg Leu Arg Geg Val Glu Glu Leu Thr. 14. McDaniel. pro Leu Val Leu Pro Ala Val Arg Pho Ann Met Ala Ser Lya Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lya Val Ala Thr. Thr. Gly Lya 17. Wild Lab. PROAFF Res Lou Arg Glu Clu Leu Val Leu Lya Ala Ala Ala Arg Ala Ser Leu Ala Thr. Gly Ile Arg Ala Gly Ile Ile Lya Val Ala Thr. Thr. Gly Lya 17. McDaniel. pro Ala Thr. Pro Pha Gln Glu Leu Val Leu Lya Ala Ala Arg Ala Ser Leu Ala Thr. Gly Val Pro Val Thr. Thr. His Thr. Ala Ala Ser 20. Wild Lab. PROALs Thr. Pro Pha Gln Glu Leu Val Leu Lya Ala Ala Arg Ala Ser Leu Ala Thr. Gly Val Pro Val Thr. Thr. His Thr. Ala Ala Ser 17. Serdar. pro Ala Thr. Pro Pha Gln Glu Leu Val Leu Lya Ala Ala Arg Ala Ser Leu Ala Thr. Gly Val Pro Val Thr. Thr. His Thr. Ala Ala Ser 17. Serdar. pro Ala Thr. Pro Pha Gln Glu Leu Val Leu Lya Ala Ala Arg Ala Ser Leu Ala Thr. Gly Val Pro Val Thr. Thr. His Thr. Ala Ala Ser 17. Serdar. pro Gln Arg Asp Gly Glu Arg Gly Arg Pro Pro Pho Leu Ser Pro Lya Leu Glu Pro Ser Arg Val Cya Ile Gly His Ser Asp Asp Thr. Asp 23. Wild Lab. PROGlin Arg Asp Gly Glu Arg Ala Ala Ala Ala Ala Ala Ala Arg Ala Ser Leu Ala Thr. Gly Val Pro Val Thr. Thr. His Thr. Ala Ala Ser 20. Serdar. pro Gln Arg Asp Gly Glu Arg Ala Ala Ala Ala Ala Ala Ala Ala Arg Ala Ser Leu Ala Thr. Gly Val Pro Val Thr. Thr. His Thr. Ala Ala Ser 20. Serdar. pro Gln Arg Asp Gly Glu Arg Ala
Wild Lab. PROAFF Ala Arg Ris Ala Gly Wei Arg Provide Fell wait Arg Wei Arg Tir Pro Respect Birly Not Asp tel Ger Lew Law Ala City Wei Arg Ser Tyr Lew Ala Ala Thr Gly Lew Trp Pho Asp Pro Pro Lew Ser Met Arg Lew Arg Tyr Val Glw Glw Lew Thr 14. Wild Lab. PROAFF Ala Arg Arg Arg Ser Tyr Lew Ala Ala Thr Gly Lew Trp Pho Asp Pro Pro Lew Ser Met Arg Lew Arg Tyr Val Glw Glw Lew Thr 14. Wild Lab. PROAFF Ala Ala Arg Ala Ala Ala Thr Gly Lew Trp Pho Asp Pro Pro Lew Ser Met Arg Lew Arg Ser Val Glw Glw Lew Thr 14. McDaniel. pro Lew Val Lew Pro Ala Vol Arg Pho Ash Met Ala Ser Lys Tyr Thr Gly Ile Arg Ala Gly Ile Ile Lye Val Ala Thr Thr Gly Lys 17. Wild Lab. PROAFF Ala Free Res Low Arg Glw Clw Life Tyr Gly Vie Glw Ess — Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys 14. McDaniel. pro Gin the Res Low Arg Glw Clw Life Tyr Gly Vie Glw Ess — Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys 17. McDaniel. pro Ala Thr Pro Pha Gln Glw Lew Val Lew Lys Ala Ala Ala Arg Ala Ser Lew Ala Thr Gly Vol Pro Val Thr Thr His Thr Ala Ala Ser 20. Wild Lab. PROAFF Thr Pro Pha Gln Glw Lew Val Lew Lys Ala Ala Ala Arg Ala Ser Lew Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 17. Serdar pro Ala Thr Pro Pha Gln Glw Lew Val Lew Lys Ala Ala Ala Arg Ala Ser Lew Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 17. Serdar pro Ala Thr Pro Pha Gln Glw Lew Val Lew Lys Ala Ala Ala Arg Ala Ser Lew Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 17. Serdar pro Gln Arg Asp Gly Glw Arg Gly Arg Pro Pro Phe Lew Ser Pro Lys Lew Glw Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23. Wild Lab. PROGin Arg Asp Gly Glw Arg Gly Arg Pro Pro Phe Lew Ser Fro Lys Lew Glw Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23. McDaniel pro Asp Lew Ser Tyr Lew Thr Ala Lew Lew Arg Gly Tyr Lew Ile Gly Lew Asp His Ile Pro His Ser Ala Ile Gly Lew Glw Asp Asn 25. McDaniel pro Asp Lew Ser Tyr Lew Thr Ala Lew Lew Arg Gly Tyr Lew Ile Gly Lew Asp His Ile Pro His Ser Ala Ile Gly Lew Glw Asp Asn 25.
McDaniel.proAls Gly Cys Arg Arg Ser Tyr Leu Als Als Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Tyr Val Glu Glu Leu Thr 14. Wild Lab. PROALS Als Als Als Als Als Thr Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu Glu Leu Thr 14. Serdar.pro Art Als Als Als Val Arg Phe Asp Met Als Ger Lys Tyr Thr Gly Ile Arg Als Gly Ile Ile Lys Val Als Thr Thr Gly Lys 17. Wild Lab. PROGET The This Leu Arg Time Ile Clu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu Glu Leu Thr 14. McDaniel.pro Gli the The Leu Val Leu Val Arg Phe Asp Met Als Ger Lys Tyr Thr Gly Ile Arg Als Gly Ile Ile Lys Val Als Thr Thr Gly Lys 17. Wild Lab. PROGET The The Lou Arg Glu Clu Leu Val Leu Lys Als Als Arg Als Ser Leu Als Thr Gly Ile Arg Als Gly Ile Ile Lys Val Als Thr Thr Gly Lys 17. McDaniel.proAls Thr Pro Phe Gln Glu Leu Val Leu Lys Als Als Arg Als Ser Leu Als Thr Gly Val Pro Val Thr Thr His Thr Als Als Ser 20. Wild Lab. PROALs Thr Pro Phe Gln Glu Leu Val Leu Lys Als Als Als Arg Als Ser Leu Als Thr Gly Val Pro Val Thr Thr His Thr Als Als Ser 17. Serdar.pro Als Thr Pro Phe Gln Glu Leu Val Leu Lys Als Ala Als Arg Als Ser Leu Als Thr Gly Val Pro Val Thr Thr His Thr Als Als Ser 17. Serdar.pro Als Thr Pro Phe Gln Glu Leu Val Leu Lys Als Ala Als Arg Als Ser Leu Als Thr Gly Val Pro Val Thr Thr His Thr Als Als Ser 20. McDaniel.proGin Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 20. Serdar.pro Gln Arg Asp Gly Glu Gli Gli Als Als Als Als Als Ser Gli Gli Leu Asp His Ile Pro His Ser Als Ile Gly Leu Glu Asp Asn 23. McDaniel.proAsp Leu Ser Tyr Leu Thr Als Leu Lou Arg Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Als Ile Gly Leu Glu Asp Asn 23. McDaniel.proAsp Leu Ser Tyr Leu Thr Als Leu Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Als Ile Gly Leu Glu Asp Asn 23.
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Wild Lab. PROALS The Pro Phe Gle Glu Leu Vai Leu Lys Ala Ala Arg Ala Sor Leu Ala The Gly Val Pro Val The The His The Ala Ala Sor 17 Serdar pro Ala The Pro Phe Gle Glu Leu Val Leu Lys Ala Ala Arg Ala Sor Leu Ala The Gly Val Pro Val The The His The Ala Ala Sor 20. McDaniel proGle Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ila Gly His Ser Asp Asp The Asp 23: Wild Lab. PROGLe Arg Asp Gly Glu Gli Gli Ala Ala Ala Ala Ala Ala Cys Clu Gli Gly Leu Ned Pro Ser Arg Val Cys Ila Gly His Ser Asp Asp The Asp 20' Serdar pro Gle Arg Asp Gly Glu Gli Gli Ala Ala Ala Ala Ala Ala Cys The Gly His Ser Asp Asp The Asp 23. McDaniel proAsp Leu Ser Tyr Leu The Ala Leu Lou Arg Gly Tyr Leu Ila Gly Leu Asp His Ila Pro His Ser Ala Ila Gly Leu Glu Asp Ase 25 Wild Lab. PROAsp Leu Ser Tyr Leu The Ala Leu Kar Ala Arg Gly Tyr Leu Ila Gly Leu Asp His Ila Pro His Ser Ala Ila Gly Leu Glu Asp Ase 25
Wild Lab. PROALS The Pro Phe Gle Glu Leu Vai Leu Lys Ala Ala Ala Arg Ala Sor Leu Ala The Gly Val Pro Val The The His The Ala Ala Sor 17 Serdar pro Ala The Pro Phe Gle Glu Leu Val Leu Lys Ala Ala Ala Arg Ala Sor Leu Ala The Gly Val Pro Val The The His The Ala Ala Sor 20. McDaniel proGle Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp The Asp 23. Wild Lab. PROGLe Arg Asp Gly Glu Arg Gly Arg Pro Pro Phe Leu Ser Fro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp The Asp 20. Serdar pro Gle Arg Asp Gly Glu The Ala Leu Lou Arg Pro Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp The Asp 23. McDaniel proAsp Leu Ser Tyr Leu The Ala Leu Lou Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Ase 23. Wild Lab. PROAsp Leu Ser Tyr Leu The Ala Leu Lou Arg Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Ase 23.
Serdar.pro Ala Thr Pro Pha Gln Glu Lou Val Leu Lya Ala Ala Ara Ala Ser Leu Ala Thr Gly Val Pro Val Thr Thr His Thr Ala Ala Ser 20. McDaniel.proGin Arg Asp Gly Glu Arg Gly Arg Pro Pro Pha Leu Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ila Gly His Ser Asp Asp Thr Asp 23: Wild Lab.PRoGin Arg Asp Gly Glu Gin Ala Ala Ala Ala Ala Ala Cys Leu Glu Pro Ser Arg Val Cys Ila Gly His Ser Asp Asp Thr Asp 20: Serdar.pro Gln Arg Asp Gly Glu Gin Ala Ala Ala Ala Ala Cys Ila Gly His Ser Asp Asp Thr Asp 23. McDaniel.proAsp Lau Ser Tyr Lau Thr Ala Lau Lou Arg Gly Tyr Lau Ila Gly Lau Asp His Ila Pro His Ser Ala Ila Gly Lau Glu Asp Asn 26: Wild Lab.PRoAsp Lau Ser Tyr Lau Thr Ala Lau Ala Arg Gly Tyr Lau Ila Gly Lau Asp His Ila Pro His Ser Ala Ila Gly Lau Glu Asp Asn 23:
McDaniel.proGin Arg Asp Gly Glu Arg Gly Arg Pro Pro Pho Lou Ser Pro Lys Leu Glu Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23: Wild Lab.PROGin Arg Asp Gly Glu Gin And All All All And Asp Cly Glu Gin And Asp Cly Glu Gin All All Asp Cly Glu Gin Asp Asp Thr Asp 20: Serdar.pro Gln Arg Asp Gly Glu Gin Gin All All Asp Asp Thr Asp 23: McDaniel.proAsp Leu Ser Tyr Leu Thr Als Leu Lou Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 25: Wild Lab.PROAsp Leu Ser Tyr Leu Thr Als Leu Asp Asp Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 23:
Wild Lab. PROGIN Arg Asp Gly Glu Glassian Alastic Pho Gly Ser Gill Gly Leu New Pro Ser Arg Val Cyo Ile Gly His Ser Asp Asp Thr Asp 20' Serdar. pro Gln Arg Asp Gly Glu Glim Glim Alastic Pho Glim Ser Glim Pro Ser Arg Val Cyo Ile Gly His Ser Asp Asp Thr Asp 23. McDaniel. pro Asp Leu Ser Tyr Leu Thr Ala Leu Lou Thr Ala Leu Lou Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 26 Gild Lab. PRo Rap Leu Ser Tyr Leu Thr Ala Leu Gly Asp Asn 23
Serdar.pro Gin Arg Asp Gly Glu Min Min Min Min Min Min Ser (Silve) Leu Men Pro Ser Arg Val Cys Ile Gly His Ser Asp Asp Thr Asp 23. McDaniel.pro Asp Leu Ser Tyr Leu Thr Ala Leu Lou arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ala Ile Gly Leu Glu Asp Asn 26 wild Lab.fRo Asp Leu Ser Tyr Leu Thr Ala Leu Glu Asp Asn 23.
McDaniel. pro Asp Leu Ser Tyr Leu Thr Ale Leu Lou Thr Ale Leu Lou Thr Gly Tyr Leu Ile Gly Leu Asp His Ile Pro His Ser Ale Ile Gly Leu Glu Asp Asn 26 Wild Lab. PRo hap Leu Ser Tyr Leu Thr Ale Leu Rig Arg Gly Tyr Leu Ile Gly Leu Asp His Ile Pro his Ser Ale Ile Gly Leu Glu Asp Asn 23
Wild Lab. FRohap Leu Ser Tyr Leu Thr Ale Leu Thr Aid Are Gly Tyr Leu Ile Cly Leu Aep Hie Ile Fro His Ser Ale Ile Gly Leu Glu Asp Asn 23
Wild Lab. FRohap Leu Ser Tyr Leu Thr Ale Leu Thr Aid Are Gly Tyr Leu Ile Cly Leu Aep Hie Ile Fro His Ser Ale Ile Gly Leu Glu Asp Asn 23
•
McDaniel.proAla Ser Ala Ser Fro Leu Leu Gly Ile Arg Ser Trp Gln Thr Arg Ala Leu Leu Ile Lys Ala Leu Ile Arp Gln Gly Tyr Met Lys Gln 29
Wild Lab. FROALS Ser Als Ser Als Ser Equ Lou Cau the tip Gin The Arg Als Lou Lou Ile Lys Als Lou Ile Asp Gin Gly Tyr Met Lys Gin 26'
Sordar.pro Als Ser Als Ser Als Ser All Lou Lou Cly He Arg Ser Trp Gin Thr Arg Als Lou Lou He Lyo Als Lou He Asp Gin Gly Tyr Mer Lyo Gin 29.
McDaniel.pro Ite Leu Val Ser Asn Asp Trp Leu Phe Cly Phe Ser Ser Tyr Val Thr Asn Ile Met Asp Val Ket Asp Arg Val Asn Pro Asp Gly Net 32
Wild Lab. PROIIs Leu Val Ser Asn Asp Trp Leu the Gly Phe Ser Ser Tyr Val Thr Asn IIe Not Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 29
Serdar, pro Ile Lou Val Ser Asn Asp Trp Leu Phe Gly Phe Ser Sor Tyr Val Thr Asn Ile Met Asp Val Met Asp Arg Val Asn Pro Asp Gly Met 32.
McDaniel.pro Ala Phé Ilo His
Wild Lab. PROAls Pho Ile Rem Lou Arg Val Ile Pro Pho Lou Arg Glu Lys Cly Val Pro Glu Glu Thr Leu Ala Gly Ile Thr Val Thr Asn Pro Ala 32
Sardar.pro Alo Phe Ile Red Lou Arg Val Ile Pro Phe Leu Arg Glu Lya Gly Val Pro Gln Glu Thr Leu Ala Gly Ile Thr Val Thr Asn 9to Ala 35.
McDanigl.pro
Wild Lab. PROArg Phe Leu Ser Pro Thr Leu Arg Ala Ser 33"
Sordar.pro Arg Phe Leu Sor Pro Thr Leu Arg Ala Ser 36.

Decoration 'Decoration #1': Shade (with black at 10% fill) residues that differ from McDaniel.pro.

Decoration 'Decoration #2': Box residues that differ from McDaniel.pro.

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ATGCAAACOUGAAGGGTTGTGCTC/
                                    CTGCGGCCGC---GAGAACTOT McDaniol D
   wild lab opu...oq
   GUTCGGCGGCCTGGCTGGGTGCGCGA-CGTGGCTGGATCGATCGACAG McDeniol P diminu
   TCGATCCGCACAC MLLa Lab opd.seq
  CCCATCCGAFCAATAC - GTSCGCG - TGCTATGACAATCTCTGAAGCGGGT McDaniel P diming.
  GCGATCAGCATCAATACBGTGCGCGGTCCTATCACAATCTCTGAAGCGGGTWILd lab ppd.meq
GCGATCAGATCAATACBGTGCGCGGTCCTATCACAATCTCTGAAGCGGTSendar.seq
TTCACACTUACTCACCACRACATCTQCCGCACCTCGGCAGGATTCTTCG WIld lab opd.seq
194 POCTEGGCCAGAGTECTTCGGTAGC-CCARACCTCTAGCGGAAAAGCCCTG Medaniel F dimino
   TECTTE CCC AGA GT T C T T C G G T A G C MG C A A A G C T C T A G C G G A A A A G G C T G Mild lab opd.aveg T G C T T G G C C A G A G T T C T T C G G T A G C MG C A A A G C T C T C G G C G A A A A G C C T G Berday.seq
243 TORGROUNT TOCOC ---GCCAGROCGGCTGGCGTGCCARCATTGTCGAT McDaniel P distau
107 TGAGACHATTECGERMANGGCCABACGGCTGGCGTGGGALCGATTGTCGAF Wild leb opd. 244
200 GTGTCGACTTTCGATATCGGTCGCGACGTCAGTTTATTGGCCGAGGTTTC McDaniel P distinu
101 GTGTCGACTTTCGATATCGGTCGCGAGGTCAGTTTATTGGCCGAGGTTTU Berdat, awq
140 GUGGGCTGCCAACGTTCATATC-TGGCGGCCACGGCCTTGTGGTCGACC McCaniel P diminu
267 CCCGGCTGCCGACCTTCATATCMTGGCGGCGACCGGCTTCTGGTTCGACC McCaniel P diminu
351 GCGGGCTGCCGACGTTCATATCMTGGTGGCGGCGACCGGCTTGTGGTTCGACC Serdar.soq
317 CCCCACTTTCGATACGATTCAGGAATGTAGAGGAACTCACACMACTTCTT MAId lab opd.seq
439 CCTGCGGTCAGATTCAATATCGCATCCGAACTACACCGGAATTAGGGCCCC McConiol F diminor
366 CCTGCGGTGACATTCAATATGGCATCGAAGGACACCGGAAATTAGGGCCGG Mild lab opc.seq
450 CCTGCGGTGAGATTCAATATCGCATCGAAGGACACCGGAATTAGGGCCGG Mild lab opc.seq
489 CATTATCAAGGTCGCGACCACAGGCAAGGCGACCCCCTTTCAGGAGTTAG McDapiel P diming
414 CAPTATCAAGGTCGCGAGCACAGGCAAGAGCGAGCGCCTTTCCAGGAGTTAC WILd lap opd.seq
138 PARTALARCEBECCECEEEGGCCACCTTGGCCACCGGTGTTCCGGTALCC McDeniel P 41mlm
ter Tellanneegeecccccagaccascttagccaccaatttagccaccaattagcattalec Serdar.soq
314 ACTCACACGGCAGCAAGTCAGCGCGATGGTGAGCAAAAGCAACGCGCGAT7 Wild lab opd.soq
598 ACTCACAGGGCAGCAAGTCAGCGGGATGGTGAGCAAGGCACCATT Serder.seq
dis frightic cohhe correspect - for cocataretre tracet creek a McDeniel P diminu.
  487 TGATACTGACGATTTGAGCTATCTCACOGCCCT-GCTGCGCG--GATACO McDantel P diminu
  TGATACTGACGATITGAGCTATET ACCGCCCTTGGCTCCCCGGGGGATACC Mild leb opd.ooq
TGATACTGACGATITGAGCTATGTGACCGCCCTTGGCTGCCCGGGGGATACC Mild leb opd.ooq
734 TEATEGOTETAGACOACATECCOCACACTECGATTCGTCTAGAAGATAAT McDaniel P dimino
   TCATCGGTGTAGACCACATGGGGGCACAGTGGCATTGGTCTAQAAGATAAT Mild lab opd.smq
   TEATEGGTETAGACCACATEE CGCACAGTGCGATTCGTCTAGAAGATAAT Serdar. seq
TIE GCGRATACHTCAMARTETTCTCTTOGGCATCCGTTCGTCAAACACGGGCTCT Mild lab opg.seq
834 CTTOATCAAGGGGCTCATGGACCAAGGCTAGATGAAACAAATCCTCGTTT McDaniol & dimino
762 CTTCATCAAGCCGCTCATCGACCAAGGCTACATGAACLAATCGTCGTTTT Rild lab opd.and
934 GTCATGGATCGCGTGAACCCCCACGGGATGGCCTTCATTC-ACTGAGAGT MeDaniel P diminu
1012 TO A CTOTOA CTAACCC QOCOCOOT FOT OT CACCOACTTOCCC FG C - - Madahled P dimino
poc.bgs del bille
1095 A 7 G A
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Decoration 'Decoration W1': Shade (with black on 10% fill) residues that differ from Econici P diminute.coq.

Decoration 'Decoration 92': Now residues that differ from HoDeniel P diminuta.seq.

Works Cited

McDaniel P. diminuta:

McDaniel, C.S., Harper, L.L. and Wild, J.R., Cloning and sequencing of a plasmid-borne gene (opd) encoding a phosphotriesterase, J. Bacteriol. 170 (5), 2306-2311 (1988). Gene Bank Accession Number: M20392

Oph-lab RC: Wild lab DNA sequence

Serdar: Serdar Sequence obtained from United States Patent and Trademark Office (uspto.gov) Patent Number 5,484,728

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Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	t	Query		
No.	Score	e Matc	h Length DB ID	Description
·				
1	1693	99.7	365 2 A43720	parathion hydrolas
2	913	53.8	325 2 A28214	phosphotriesterase
3	448	26.4	326 2 D70962	hypothetical prote
4	408	24.0	314 2 F90424	hypothetical prote
5	385	22.7	323 2 E75459	probable phosphotr
6	331	19.5	305 2 AB1321	probable phosphotr
7	309	18.2	331 2 A83678	hypothetical prote
8	308	18.1	292 2 F65132	hypothetical 32.9
9	296	17.4	679 2 F83723	hypothetical prote
10	277.5	16.3	355 2 AD2933	hypothetical prote
11	277.5	16.3	355 2 C98349	resiniferatoxin-bi
12	273	16.1	344 2 AC0994	puative phophotrie
13	269.5	15.9	330 2 AG1405	Phosphotriesterase
14	268.5	15.8	330 2 AG1781	Phosphotriesterase
15	229	13.5	351 2 A99586	conserved hypothet

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RESULT 1
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A43720

parathion hydrolase precursor - Flavobacterium sp. (ATCC 27551)

C;Species: Flavobacterium sp.

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 08-Oct-1999

C:Accession: A43720

R; Mulbry, W.W.; Kams, J.S.

J. Bacteriol. 171, 6740-6746, 1989

A;Title: Parathion hydrolase specified by the Flavobacterium opd gene: relationship

between the gene and protein.

A;Reference number: A43720; MUID:90078122; PMID:2556372

A;Accession: A43720
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 < MUL>

A;Cross-references: GB:M29593; NID:g148712; PIDN:AAA24930.1; PID:g148713

A; Experimental source: ATCC 27551

Query Match 99.7%; Score 1693; DB 2; Length 365;

Best Local Similarity 100.0%; Pred. No. 1.1e-126;

Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2

SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61

Db 30

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89

Qy 62

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121

Db 90

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Db 150

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Qy 182

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Db 210

EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 269

Qy 242

ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 301

Db 270

ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 329

Qy 302 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 337

Db 330 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 365

Database : A_Geneseq_29Jan04:*
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 3: geneseqp2000s:*
 4: geneseqp2001s:*
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 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1693	99.7	365	2	AAR05573	Aar05573 Parathion
4	1693	99.7	365	6	ABB82802	Abb82802 Flavobact
5	1689	99.5	336	6	ABG72650	Abg72650 Flavobact
6	1686	99.3	357	2	AAY43487	Aay43487 Amino aci
7	1685	99.2	334	2	AAY43486	Aay43486 Amino aci
8	1558	91.8	356	6	ABB82799	Abb82799 A. radiob
9	1558	91.8	384	6	ABB82798	Abb82798 A. radiob
10	1552	91.4	384	6	ABB82801	Abb82801 A. radiob
11	1535	90.4	384	6	ABB82800	Abb82800 A. radiob
12	465	27.4	326	6	ABU33918	Abu33918 Protein e
13	448	26.4	326	6	ABU36432	Abu36432 Protein e
14	400	23.6	306	6	ABU34486	Abu34486 Protein e
15	372.5	21.9	346	6	ABU31613	Abu31613 Protein e
16	331	19.5	305	5	ABB48499	Abb48499 Listeria
17	331	19.5	305	6	ABU32460	Abu32460 Protein e
18	308	18.1	292	6	ABU14978	Abul4978 Protein e
19	. 283	16.7	345	6	ABU21704	Abu21704 Protein e
20	273	16.1	344	6	ABU47684	Abu47684 Protein e
21	273	16.1	344	6	ABU47288	Abu47288 Protein e
22	269.5	15.9	330	5	ABB47719	

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DT
     12-DEC-2002 (first entry)
XX
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DE
XX
KW
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KW
     chemical warfare; pesticide; pollutant; detoxification; decontamination.
XX
os
     Unidentified.
XX
FH
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                     /label= Signal peptide
FT
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FT
                     /label= Mature protein
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     06-SEP-2002.
XX
PF
     21-FEB-2002; 2002WO-US005755.
XX
PR
     21-FEB-2001; 2001US-00791138.
PR
     20-FEB-2002; 2002US-00081737.
XX
PA
     (BATT ) BATTELLE MEMORIAL INST.
XX
ΡI
     Ackerman EJ, Liu J, Chenghong L;
XX
DR
     WPI; 2002-713364/77.
DR
     N-PSDB; ABO81428.
XX
PT
     Protein system, for facilitating chemical reactions e.g. hydrolysis,
PT
     oxidation, hydrogenation and proteolysis, comprises porous matrix
PΤ
     material and protein within matrix.
XX
PS
     Example; Fig 4; 56pp; English.
XX
CC
     The present sequence is the protein sequence of an organophosphorous
CC
     hydrolase (OPH) encoded by an expression plasmid of the invention. The
CC
     invention provides a method for producing OPH by transfecting a host cell
CC
     with a vector comprising a sequence encoding OPH linked to a T7
CC
     expression control sequence, culturing the transfected host cell, and
CC
     purifying OPH from the cell or culture medium. This OPH has an activity
CC
     of about 13,000 U/mg. The host cell can be prokaryotic, e.g. Escherichia
CC
     coli, or eukaryotic, e.g. Pichia pastoris. The invention also provides a
CC
    protein system for facilitating chemical reactions. The protein system
CC
     comprises a porous matrix material having a pore volume of which at least
CC
     90% is composed of pores of 50-400 Angstroms. The protein occupies 5-40%
CC
    of the average pore volume, and is preferably an enzyme, especially OPH
CC
    having an activity of 60-95% that of the active state and retaining about
CC
    10% of its activity after 24 hr under alkaline conditions. The porous
```

```
CC
    matrix may comprise surface hydroxyls that are reacted with a coupling
    agent to form a functionalised monolayer. The system provides high enzyme
CC
CC
    activities on a porous support, stability under a variety of conditions,
CC
    high densities of active protein and capability in industrial-scale
    applications. It provides environmentally safe methods of destroying
CC
CC
    chemical weapons and organophosphorous pesticides while avoiding the
    dangers inherent in burning these materials. It can be used in filtration
CC
CC
    equipment for individual soldiers and pesticide workers, and in vehicles,
CC
    aircraft, ships and buildings such as civilian and military defence
CC
    shelters, to perform detoxifications
XX
SQ
    Sequence 337 AA;
 Query Match
                     99.8%; Score 1695; DB 5; Length 337;
 Best Local Similarity
                     99.7%; Pred. No. 1.1e-163;
 Matches 336: Conservative
                           1: Mismatches
                                          0: Indels
                                                                0:
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Qу
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Db
Qу
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           Db
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Qy
           Db
        181 GEQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASA 240
        241 SALLGIRSWOTRALLIKALIDOGYMKOILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFI 300
QУ
           241 SALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFI 300
Db
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Qу
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301 PLRVIPFLREKGVPQQTLAGITVTNPARFLSPTLRAS 337

Db

Database : SPTREMBL 25:* 1: sp_archea:* 2: sp_bacteria:* 3: sp fungi:* 4: sp_human:* 5: sp_invertebrate:* sp_mammal:* 6: 7: sp_mhc:* 8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_rvirus:* 16: sp_bacteriap:* 17: sp_archeap:*

.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
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1	1688	99.4	365	2	Q8GC45	Q8gc45 flavobacter
2	1630	96.0	365	2	Q8VLR0	Q8vlr0 chryseobact
3	1558	91.8	384	2	Q93LD7	Q93ld7 agrobacteri
4	915	53.9	325	2	Q47934	Q47934 flavobacter
5	448	26.4	326	16	Q7U2I4	Q7u2i4 mycobacteri
6	408	24.0	314	17	Q97VT7	Q97vt7 sulfolobus
7	385	22.7	323	16	Q9RVU2	Q9rvu2 deinococcus
8	331	19.5	305	16	Q8Y5T5	_ Q8y5t5 listeria mo
9	325.5	19.2	362	16	Q985I1	Q985il rhizobium l
10	309	18.2	331	16	Q9KG87	Q9kg87 bacillus ha
11	306	18.0	292	16	Q8FCW5	Q8fcw5 escherichia
12	304	17.9	292	16	Q7UAS1	Q7uas1 shigella fl
13	296	17.4	679	16	Q9KF95	Q9kf95 bacillus ha
14	288	17.0	344	16	Q8FG90	Q8fg90 escherichia
15	277.5	16.3	355	16	Q8UBF0	Q8ubf0 agrobacteri
16	273	16.1	344	16	Q8XFU6	Q8xfu6 salmonella
17	270.5	15.9	349	13	Q7SZS2	Q7szs2 xenopus lae
18	269.5	15.9	330	16	Q8Y427	Q8y427 listeria mo
19	268.5	15.8	330	16	Q927J1	Q927j1 listeria in

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                                      365 AA.
AC
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    01-MAR-2003 (TrEMBLrel. 23, Created)
DΤ
    01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Parathion hydrolase precursor (EC 3.1.8.1).
GN
OS
    Flavobacterium sp. ATCC 27551.
OG
    Plasmid pPDL2.
OC
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OC
    Flavobacteriaceae: Flavobacterium.
OX
    NCBI TaxID=74567;
RN
    [1]
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    SEQUENCE FROM N.A.
RC
    STRAIN=ATCC 27551;
RA
    Siddavatam D., Manavathi B., Merrick M.;
    "The conserved region surrounding the organophosphorus pesticide
RT
RT
    degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the
RT
    features of a complex transposon.";
RL
    Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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DR
    GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR
    GO; GO:0008270; F:zinc ion binding; IEA.
DR
    GO; GO:0009056; P:catabolism; IEA.
    InterPro; IPR000437; Prok lipoprot S.
DR
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    InterPro; IPR001559; PTE.
DR
    Pfam; PF02126; PTE; 1.
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DR
    PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
DR
KW
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FT
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SO
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DT
    01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT
    01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE
    Parathion hydrolase precursor (EC 3.1.8.1).
GN
os
    Chryseobacterium balustinum.
OG
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OC
    Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
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OX
    NCBI TaxID=246;
RN
    [1]
    SEQUENCE FROM N.A.
RP
RA
    Siddavatam D., Manavathi B., Merrick M.;
RT
    "The conserved region surrounding the organophosphorus pesticide
RT
    degrading (opd) gene on the Flavobacterium plasmid pPDL2 has the
    features of a complex transposon.";
RT
    Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR
    EMBL; AJ426431; CAD19996.1; -.
    GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR
    GO; GO:0004063; F:aryldialkylphosphatase activity; IEA.
DR
    GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR
DR
    GO; GO:0008270; F:zinc ion binding; IEA.
    GO; GO:0009056; P:catabolism; IEA.
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    InterPro; IPR001559; PTE.
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    Pfam; PF02126; PTE; 1.
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    PROSITE; PS01322; PHOSPHOTRIESTERASE 1; 1.
DR
    PROSITE; PS01323; PHOSPHOTRIESTERASE 2; 1.
KW
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FT
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                 1
                      29
                               POTENTIAL.
FT
    CHAIN
                30
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                               PARATHION HYDROLASE.
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Db	
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Database: Issued_Patents_AA:*

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1689	99.5	, 336	4	US-09-603-450-4	Sequence 4, Appli
2	1688	99.4	365	6	5484728-2	Patent No. 5484728
3	267	15.7	352	4	US-09-543-681A-8100	Sequence 8100, Ap
4	238.5	14.0	349	1	US-08-343-027A-12	Sequence 12, Appl
5	105	6.2	477	4	US-09-489-039A-9937	Sequence 9937, Ap
6	104	6.1	495	4	US-09-252-991A-21509	Sequence 21509, A
7	99.5	5.9	2482	4	US-09-252-991A-16967	Sequence 16967, A
8	92	5.4	908	4	US-09-328-352-7168	Sequence 7168, Ap
9	91.5	5.4	461	4	US-09-134-000C-5551	Sequence 5551, Ap
10	90.5	5.3	647	4	US-09-725-735A-18	Sequence 18, Appl
11	90	5.3	569	4	US-09-543-681A-5106	Sequence 5106, Ap
12	89.5	5.3	1161	4	US-09-252-991A-22872	Sequence 22872, A
. 13	89	5.2	403	4	US-09-252-991A-25706	Sequence 25706, A
14	89	5.2	655	4	US-09-107-532A-4425	Sequence 4425, Ap
15	88.5	5.2	283	4	US-09-543-681A-8240	Sequence 8240, Ap
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17	87	5.1	476	4	US-09-489-039A-14013	Sequence 14013, A

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RESULT 1
US-09-603-450-4
; Sequence 4, Application US/09603450
; Patent No. 6469145
; GENERAL INFORMATION:
; APPLICANT: Rastogi, Vipin K
; APPLICANT: Cheng, Tu-c
 APPLICANT: DeFrank, Joseph J
  TITLE OF INVENTION: One-Step Purification Process for Organophosphorus
  TITLE OF INVENTION: Hydrolase Enzyme
 FILE REFERENCE: DAM-508-99
  CURRENT APPLICATION NUMBER: US/09/603,450
  CURRENT FILING DATE: 2000-06-26
 NUMBER OF SEO ID NOS:
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; SEQ ID NO 4
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   TYPE: PRT
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Database :

SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
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1	1693	99.7	365	1	OPD_FLASP	P16648 flavobacter
2	448	26.4	326	1	PHP_MYCTU	P96413 mycobacteri
3	308	18.1	292	1	PHP_ECOLI	P45548 escherichia
4	243.5	14.3	349	1	PTER_HUMAN	Q96bw5 homo sapien
5	242.5	14.3	349	1	PTER_RAT	Q63530 rattus norv
6	239.5	14.1	349	1	PTER_MOUSE	Q60866 mus musculu
7	211.5	12.5	350	1	PTER DROME	Q9vhf2 drosophila
8	127	7.5	216	1	YE97 MYCPN	P75290 mycoplasma
9	103	6.1	226	1	GPH2_PSEAE	Q9hz62 pseudomonas
10	103	6.1	319	1	HE31_STRCO	Q9wx16 streptomyce
11	96	5.7	342	1	ARGC_STRCO	P54895 streptomyce
12	93.5	5.5	352	1	TFTE_BURCE	Q45072 burkholderi
13	93	5.5	3421	1	TEGU_HSVEB	P28955 equine herp
14	92.5	5.4	522	1	LEU1 DEIRA	Q9rua9 deinococcus
15	92.5	5.4	898	1	SYA_METTH	O27718 methanobact
.16	92	5.4	486	1	LE11_PYRAB	Q9uz08 pyrococcus
. 17	92	5.4	617	1	VATA_MANSE	P31400 manduca sex
18	91.5	5.4	494	1	TYRO_RHIME	P33180 rhizobium m
19	91.5	5.4	520	1	LEU1_YERPE	Q8zig8 yersinia pe
20	91.5	5.4	1139	1	VRNA_BSMV	P17595 barley stri
21	91	5.4	1290	1	RPOC_MYCPN	P75271 mycoplasma
22	90.5	5.3	333	1	YF72_HALN1	Q9hpl8 halobacteri
23	90.5	5.3	838	1	GLGB_STRAW	Q82jf0 streptomyce
24	89.5	5.3	300	1	Y505_MYCLE	Q49823 mycobacteri
25	89.5	5.3	308	1	Y505_MYCTU	Q11169 mycobacteri
26	89.5	5.3	435	1	PROA_BRAJA	Q89x85 bradyrhizob
27	89.5	5.3	958	1	GCP2_PSEAE	Q9htx7 pseudomonas
28	89	5.2	614	1	VAA2_DROME	Q27331 drosophila

```
RESULT 1
OPD FLASP
                    STANDARD;
                                   PRT;
     OPD FLASP
                                          365 AA.
     P16648; P13739;
AC
ĎΤ
     01-AUG-1990 (Rel. 15, Created)
DΤ
     01-AUG-1990 (Rel. 15, Last sequence update)
     10-OCT-2003 (Rel. 42, Last annotation update)
DE
     Parathion hydrolase precursor (EC 3.1.8.1) (Phosphotriesterase)
DE
     (PTE).
GN
     OPD.
     Flavobacterium sp. (strain ATCC 27551), and
os
os
     Brevundimonas diminuta (Pseudomonas diminuta).
OG
     Plasmid pCMS1.
OC
     Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC
     Flavobacteriaceae; Flavobacterium.
OX
     NCBI TaxID=239, 293;
RN
RP
     SEQUENCE FROM N.A., AND SEQUENCE OF 30-53.
RC
     SPECIES=Flavobacterium sp ATCC 27551;
RX
     MEDLINE=90078122; PubMed=2556372;
RA
     Mulbry W.W., Karns J.S.;
RT
     "Parathion hydrolase specified by the Flavobacterium opd gene:
RT
     relationship between the gene and protein.";
RL
     J. Bacteriol. 171:6740-6746(1989).
RN
     [2]
RP
     SEQUENCE FROM N.A., AND SEQUENCE OF 30-44.
RC
     SPECIES=B.diminuta; STRAIN=MG;
RA
     Serdar C.M., Murdock D.C., Rohde M.F.;
RT
     "Parathion hydrolase gene from Pseudomonas diminuta MG: subcloning,
     complete nucleotide sequence, and expression of the mature portion of
RT
RT
     the enzyme in Escherichia coli.";
RL
     Biotechnology 7:1151-1155(1989).
RN
RP
     SEQUENCE FROM N.A.
RC
     SPECIES=B.diminuta; STRAIN=MG;
RX
    MEDLINE=88198028; PubMed=2834339;
RA
    McDaniel C.S., Harper L.L., Wild J.R.;
RT
     "Cloning and sequencing of a plasmid-borne gene (opd) encoding a
RT
    phosphotriesterase.";
RL
    J. Bacteriol. 170:2306-2311(1988).
RN
     [4]
RP
    ACTIVE SITE.
RX
    MEDLINE=94206935; PubMed=8155644;
     Kuo J.M., Raushel F.M.;
RA
RT
     "Identification of the histidine ligands to the binuclear metal
RT
     center of phosphotriesterase by site-directed mutagenesis.";
RL
    Biochemistry 33:4265-4272(1994).
RN
     [5]
RP
    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC
    SPECIES=B.diminuta;
RX
    MEDLINE=95092756; PubMed=7999757;
RA
    Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
RT
     "Three-dimensional structure of phosphotriesterase: an enzyme capable
RT
    of detoxifying organophosphate nerve agents.";
RL
    Biochemistry 33:15001-15007(1994).
RN
     [6]
RP
    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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SPECIES=B.diminuta:
RX
    MEDLINE=95315185; PubMed=7794910;
RA
    Benning M.M., Kuo J.M., Raushel F.M., Holden H.M.;
RT
    "Three-dimensional structure of the binuclear metal center of
RT
    phosphotriesterase.";
RL
    Biochemistry 34:7973-7978(1995).
RN
RP
    X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RC
    SPECIES=B.diminuta;
RX
    MEDLINE=96214508; PubMed=8634243;
RA
    Vanhooke J.L., Benning M.M., Raushel F.M., Holden H.M.;
RT
    "Three-dimensional structure of the zinc-containing
RT
    phosphotriesterase with the bound substrate analog diethyl
RT
    4-methylbenzylphosphonate.";
RL
    Biochemistry 35:6020-6025(1996).
CC
    -!- FUNCTION: Has an unusual substrate specificity for synthetic
CC
        organophosphate triesters and phosphorofluoridates. All of the
CC
        phosphate triesters found to be substrates are synthetic
CC
        compounds. The identity of any naturally occurring substrate for
CC
        the enzyme is unknown. Has no detectable activity with phosphate
CC
        monoesters or diesters and no activity as an esterase or protease.
CC
        It catalyzes the hydrolysis of the insecticide paraoxon at a rate
CC
        approaching the diffusion limit and thus appears to be optimally
CC
        evolved for utilizing this synthetic substrate.
CC
    -!- CATALYTIC ACTIVITY: Aryl dialkyl phosphate + H(2)O = dialkyl
CC
        phosphate + an aryl alcohol.
CC
    -!- COFACTOR: Binds 2 zinc ions per subunit.
CC
    -!- PATHWAY: Pesticide detoxification.
CC
    -!- SUBUNIT: Homodimer.
CC
    -!- SUBCELLULAR LOCATION: Membrane-associated.
CC
    -!- BIOTECHNOLOGY: Has attracted interest because of its potential use
CC
        in the detoxification of chemical waste and warfare agents and its
CC
        ability to degrade agricultural pesticides such as parathion.
CC
    -!- SIMILARITY: Belongs to the phosphotriesterase family.
CC
    -!- CAUTION: Ref.3 sequence differs from that shown due to multiple
CC
        sequencing errors.
CC
    -----
    This SWISS-PROT entry is copyright. It is produced through a collaboration
CC
CC
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
    the European Bioinformatics Institute. There are no restrictions on its
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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    or send an email to license@isb-sib.ch).
CC
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DR
    EMBL; M29593; AAA24930.1; -.
DR
    EMBL; M20392; AAA98299.1; ALT FRAME.
DR
    PIR; A28214; A28214.
DR
    PIR; A43720; A43720.
DR
    PDB; 1DPM; 20-AUG-97.
DR
    PDB; 1EYW; 20-DEC-00.
DR
    PDB; 1EZ2; 20-DEC-00.
DR
    PDB; 1HZY; 04-APR-01.
DR
    PDB; 110B; 04-APR-01.
DR
    PDB; 1IOD; 04-APR-01.
DR
    PDB; 1JGM; 04-JUL-01.
DR
    PDB; 1PSC; 01-APR-97.
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DR
     PDB; 1PTA; 01-DEC-95.
     InterPro; IPR000437; Prok_lipoprot_S.
DR
DR
     InterPro; IPR001559; PTE.
DR
     Pfam; PF02126; PTE; 1.
DR
     PROSITE; PS01322; PHOSPHOTRIESTERASE 1; 1.
DR
     PROSITE; PS01323; PHOSPHOTRIESTERASE 2; 1.
KW
     Hydrolase; Membrane; Plasmid; Signal; Metal-binding; Zinc;
KW
     3D-structure.
FT
     SIGNAL
                    1
                           29
FT
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                                     PARATHION HYDROLASE.
                   30
FT
     METAL
                                     ZINC 1.
                   55
                           55
FT
     METAL
                           57
                                     ZINC 1.
                   57
FT
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                  169
                          169
                                     ZINC 1 AND 2.
FT
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                  201
                          201
                                     ZINC 2.
FT
     METAL
                                     ZINC 2.
                  230
                          230
FT
     METAL
                  301
                          301
                                     ZINC 1.
FT
     STRAND
                   36
                           39
FT
     TURN
                   40
                           41
FT
     STRAND
                   42
                           45
FT
     HELIX
                   46
                           49
FT
     STRAND
                   51
                           56
FΤ
     STRAND
                   59
                           60
FT
     TURN
                   63
                           64
FT
     HELIX
                   65
                           68
FT
     HELIX
                   70
                           73
FT
     HELIX
                   76
                           92
FT
     TURN
                   93
                           94
FT
     STRAND
                   95
                          100
FT
     HELIX
                  104
                          106
FT
     TURN
                  107
                          107
FT
     HELIX
                  110
                          120
FT
     TURN
                  121
                          121
FT
     STRAND
                  123
                          125
FT
     STRAND
                  127
                          129
FT
     HELIX
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                          139
FT
     TURN
                  140
                          140
FT
     HELIX
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                          155
FT
     TURN
                  156
                          156
FT
     STRAND
                  158
                          158
FT
     TURN
                  159
                          162
FT
     STRAND
                  163
                          163
FT
     STRAND
                  167
                          171
FT
     HELIX
                  178
                          194
FT
     STRAND
                  198
                          201
     HELIX
FT
                  204
                          206
FT
     TURN
                  207
                          207
FT
     HELIX
                  208
                          218
FT
     TURN
                  219
                          220
FT
     HELIX
                  223
                          225
FT
     STRAND
                  226
                          228
FT
     HELIX
                  231
                          233
FT
     HELIX
                  237
                          246
FT
     TURN
                  247
                          247
FT
     STRAND
                  249
                          252
FT
     TURN
                  255
                          256
FT
     TURN
                  260
                          261
FT
     TURN
                  263
                          264
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FT
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             266
                   272
FT
    HELIX
             277
                   289
FT
    TURN
             290
                   291
FT
    HELIX
             293
                   295
FT
    STRAND
             296
                   298
FT
    STRAND
             305
                   306
FT
    TURN
             311
                   312
FT
    HELIX
             313
                   320
FT
    TURN
             322
                   323
FT
    HELIX
             324
                   326
FT
    HELIX
             327
                   330
FT
    TURN
             331
                   331
FT
    HELIX
             332
                   338
FT
    TURN
             339
                   340
FT
    HELIX
             343
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FT
    TURN
             351
                   351
FT
    HELIX
             352
                   358
SQ SEQUENCE
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 Best Local Similarity
                    100.0%; Pred. No. 4.1e-128;
 Matches 336; Conservative
                          0; Mismatches
                                         0: Indels
                                                    0:
                                                       Gaps
                                                              0:
Qy
         2 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 61
           30 SIGTGDRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRR 89
        62 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTOF 121
Qу
           Db
        90 ARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTOF 149
        122 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDG 181
Qу
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        150 FLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASORDG 209
        182 EQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASAS 241
Qy
        Db
QУ
        242 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 301
           270 ALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIP 329
Db
Qy
        302 LRVIPFLREKGVPOETLAGITVTNPARFLSPTLRAS 337
           Db
        330 LRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS 365
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